22. (New) A method of analyzing a nucleotide sequence of a polynucleotide of interest comprising the steps of:

a) contacting the polynucleotide of interest with a population of single-stranded primers wherein said population of single-stranded primers comprises at least two oligonucleotides of different lengths wherein said oligonucleotides have known sequences, such that at least two oligonucleotides hybridize to the polynucleotide of interest immediately adjacent to one or more nucleotides to be identified, generating template-single-stranded primer complexes;

b) subjecting said complexes to a single base extension reaction to extend each hybridized primer by a terminating nucleotide, generating extended primers;

c) separating said extended primers from each other; and

d) identifying each terminating nucleotide that has been added to each extended primer.

23. (New) The method of Claim 22, wherein the single base extension reaction comprises subjecting the annealed primers to a reaction mixture comprising a polymerase and nucleotides corresponding to each of the four different bases.

24. (New) The method of Claim 23, wherein the nucleotides corresponding to each of the four different bases are mutually distinguishable.

25. (New) The method of Claim 24, wherein three of the four nucleotides are differently labeled.

26. (New) The method of Claim 25, wherein the three differently labeled nucleotides are fluorescently labeled.

27. (New) The method of Claim 22, further comprising analyzing the sequence of the complimentary polynucleotide of interest.

28. (New) The method of Claim 22, wherein the terminating nucleotides are dideoxynucleotides.

29. (New) The method of Claim 22, wherein the length of the oligonucleotide primers is between 7 and 30 inclusive.

30. (New) The method of Claim 22, wherein the length of the oligonucleotide primers is between 20 and 24 inclusive.

31. (New) The method of Claim 22, wherein identifying the terminating nucleotide comprises the use of a charge coupled device or a photomultiplier tube.

32. (New) A method of analyzing a nucleotide sequence of a polynucleotide of interest for the presence or absence of one or more alterations, wherein the sequence of the polynucleotide of interest is generally known, comprising the steps of;

a) contacting said polynucleotide of interest with a population of single-stranded primers wherein said population of single-stranded primers comprises at least two oligonucleotides of different lengths and wherein said oligonucleotides have known sequences, such that at least two oligonucleotides hybridize immediately adjacent to said one or more alterations, if present, in the polynucleotide of interest, generating template-single-stranded primer complexes;

b) subjecting said complexes to a single base extension reaction to extend each hybridized primer by the addition of a terminating nucleotide, generating extended primers;

c) separating said extended primers from each other; and

d) identifying each terminating nucleotide that has been added to each extended primer, and

e) comparing said identified nucleotide with the sequence of the polynucleotide of interest, thereby determining the presence or absence of one or more alterations.

33. (New) The method of Claim 32, wherein the single base extension reaction comprises subjecting the annealed primers to a reaction mixture comprising a polymerase and nucleotide corresponding to each of the four different bases.

34. (New) The method of Claim 33, wherein the nucleotides corresponding to each of the four different bases are mutually distinguishable.

35. (New) The method of Claim 34, wherein three of the four nucleotides are differently labeled.

36. (New) The method of Claim 35, wherein the three differently labeled nucleotides are fluorescently labeled.

37. (New) The method of Claim 32, further comprising analyzing the sequence of the complimentary polynucleotide of interest.

38. (New) The method of Claim 32, wherein the terminating nucleotides are dideoxynucleotides.

39. (New) The method of Claim 32, wherein the length of the oligonucleotide primers is between 7 and 30 inclusive.

40. (New) The method of Claim 32, wherein the length of the oligonucleotide primers is between 20 and 24 inclusive.

41. (New) The method of Claim 11, wherein identifying the terminating nucleotide comprises the use of a charge coupled device or a photomultiplier tube.

42. (New) A method of analyzing a nucleotide sequence of a polynucleotide of interest comprising the steps of;

Sub B3

a) contacting said polynucleotide of interest to a population of single-stranded primers, wherein said single-stranded primers comprise an array of one or more sets of oligonucleotides wherein the oligonucleotides of a set differ from each other by one base at the 3' end and wherein said oligonucleotides have known sequence and wherein each said oligonucleotide having known sequence is attached to a solid support at a known location, to form the array, wherein at least one oligonucleotide of the array hybridizes to said polynucleotide of interest immediately adjacent to one or more nucleotides to be identified, generating template-single-stranded primer complexes;

b) subjecting said complexes to a single base extension reaction to extend each annealed primer by a terminating nucleotide, generating extended primers; and

c) identifying each terminating nucleotide that has been added to each primer.

43. (New) The method of Claim 42, wherein the single base extension reaction comprises subjecting the annealed primers to a reaction mixture comprising a polymerase and nucleotides corresponding to each of the four different bases.

44. (New) The method of Claim 43, wherein the nucleotides corresponding to each of the four different bases are mutually distinguishable.

45. (New) The method of Claim 44, wherein three of the four nucleotides are differently labeled.

46. (New) The method of Claim 45, wherein the three differently labeled nucleotides are fluorescently labeled.

47. (New) The method of Claim 42, further comprising analyzing the sequence of the complimentary polynucleotide of interest.

48. (New) The method of Claim 42, wherein the terminating nucleotides are dideoxynucleotides.

49. (New) The method of Claim 42, wherein the length of the oligonucleotide primers is between 7 and 30 inclusive.

50. (New) The method of Claim 42, wherein the length of the oligonucleotide primers is between 20 and 24 inclusive.

51. (New) The method of Claim 42, wherein the arrays of sets of oligonucleotide primers comprise oligonucleotide primers of different lengths.

52. (New) The method of Claim 42, wherein identifying the terminating nucleotide comprises the use of a charge coupled device or a photomultiplier tube.

53. (New) The method of Claim 42, wherein the terminating nucleotides are removed from the annealed primers after completed analysis to prepare the solid support for reuse.

REMARKS

Support for Claim Amendments

Claims 1-21 have been cancelled and new Claims 22-53 have been added. Claim 22 is drawn to a method of analyzing a nucleotide sequence of a polynucleotide of interest comprising the steps of contacting a population of single-stranded primers to said polynucleotide of interest. The population of primers comprises at least two oligonucleotides of different lengths, wherein the oligonucleotides have known sequences such that at least two oligonucleotides hybridize to the polynucleotide of interest immediately adjacent to one or more nucleotides to be identified,